

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: March 2, 2002, 20:03:35 ; Search time 157.73 Seconds

2217.642 Million cell updates/sec

Title: US-09-540-235-1

Sequence: 1 acgcccgtcattgagaatta.....acatccatctaatgttgtta 408

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 930621 seqs, 428662619 residues

Total number of hits satisfying chosen parameters: 1861242

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Minimum DB seq length: 0
Maximum DB seq length: 20000000000
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Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	130	31.9	637	21	AAC49061	Arabidopsis thaliana
2	124.2	30.4	636	21	AAC45801	Arabidopsis thaliana
3	121	29.7	638	21	AAC34600	Arabidopsis thaliana
4	118	28.9	638	21	AAC36634	Arabidopsis thaliana
5	109.8	26.9	1348	22	AAH29927	C albicans apopos
6	104.2	25.5	496	21	AAA31256	Plant microsatellit
7	102.2	25.0	788	21	AAF08074	Fusarium venenatum
8	101.2	24.8	431	22	AAI52287	Probe #20973 used
9	97.6	23.9	747	21	AAF13354	Aspergillus oryzae
10	95.8	23.5	1331	22	AAH29813	S cerevisiae apopto
11	90.4	22.2	508	21	AAC03878	Human secreted pro

C	12	87.8	21.5	785	21	AAFI5011	Trichoderma reesei
C	13	80.6	19.8	472	22	AAI39236	Probe #7922 used t
C	14	74.6	18.3	430	21	AAAC41333	Zea mays DNA fragm
C	15	73.4	18.0	629	21	AAFI13807	Aspergillus niger
C	16	71.4	17.5	579	21	AAFI1407	Aspergillus niger
C	17	70.4	17.3	358	21	AAC00996	Human secreted pro
C	18	63.2	15.5	258	22	AAI25954	Probe #15887 for g
C	19	63.2	15.5	258	22	AAI53325	Probe #2201 used
C	20	63.2	15.5	505	22	AAI16759	Probe #6692 for ge
C	21	63.2	15.5	505	22	AAI40246	Probe #8932 used t
C	22	57.8	14.2	300	22	AAI21431	Probe #11364 for g
C	23	57.8	14.2	300	22	AAI46720	Probe #15406 used
C	24	57.8	14.2	300	22	AAI07126	Probe #7117 used t
C	25	51	12.5	449	22	AAH83347	Human ovarian tumor
C	26	48.2	11.8	936	22	AAFS6252	Oligonucleotide D1
C	27	48.2	11.8	936	22	AAFS6254	Oligonucleotide D1
C	28	48.2	11.8	936	22	AAFS6257	Oligonucleotide D1
C	29	48.2	11.8	936	22	AAFS6259	Oligonucleotide D1
C	30	48.2	11.8	936	22	AAFS6262	Oligonucleotide D2
C	31	48.2	11.8	936	22	AAFS6255	Oligonucleotide D1
C	32	47.4	11.6	935	21	AAAC18519	Human secreted pro
C	33	47.4	11.6	936	21	AAFS6252	Oligonucleotide D1
C	34	47.4	11.6	936	22	AAFS6254	Oligonucleotide D1
C	35	47.4	11.6	936	22	AAFS6257	Oligonucleotide D1
C	36	47.4	11.6	936	22	AAFS6259	Oligonucleotide D2
C	37	47.4	11.6	936	22	AAFS6262	Oligonucleotide D2
C	38	47.4	11.6	938	22	AAFS6255	Oligonucleotide D1
C	39	45	11.0	205	21	AAAI1734	Plant microsatellit
C	40	44.8	11.0	465	22	AAI12233	Probe #2166 for ge
C	41	44.8	11.0	465	22	AAI33587	Probe #2273 used t
C	42	44.8	11.0	465	22	AAI02146	Probe #1237 used t
C	43	44.6	10.9	287	15	AAO76714	Human genome fragm
C	44	44	10.8	199	21	AAO10159	Human secreted pro
C	45	43	10.5	337	21	AAZ80502	Human colon cancer

RESULT	1
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ID	AAAC49069 standard; DNA; 637 BP.
XX	
AC	AAAC49069;
XX	
DT	18-OCT-2000 (first entry)
XX	
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 59811.
XX	
XX	Hybridisation assay; genetic mapping; gene expression control
KM	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
XX	
OS	Arabidopsis thaliana.
XX	
PN	EP1033405-A2.
XX	
PD	06-SEP-2000.
XX	
PE	25-FEB-2000; 2000EP-0301439.
XX	
PR	25-FEB-1999; 99US-0121825.
PR	05-MAR-1999; 99US-0123180.
PR	09-MAR-1999; 99US-0123548.
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Query Match 31.9%; Score 130; DB 21; Length 637;
Best Local Similarity 62.7%; Pred. No. 1, 1e-31;
Matches 202; Conservative 0; Mismatches 120; Indels 0; Gaps 0;

QY 87 tcagtcgcatgaagattcccaagtgtatcgctgcgtctagaagaagaaggaagca 146
DB 31 tcagcgcgcatgaagttcaatccgcgtgtcgaagctcttcgcgcggaagacaggaagct 90
QY 147 tacttcaagcacacattctctgtacacgaatatactatgcacccctgtcccaagaa 206
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QY 207 ctacgacgaataatagcggttcttcttacttcttacttgcgaagaagaagcaatatac 266
DB 151 ctccgaaacaacacacacacgacatccatccatccgattcgttaagacgaagtgcaagtt 210
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DB 211 gtccgaggagcgttcaagggaggaagaagaagggagtgagtgagtgatccgcgaagtg 270
QY 327 cggatacatatcgagagagtgaccaggaagaagaagcgaaatggaatgactgttggga 386
DB 271 gtgattcacatcgagatccacaaaggagaaagtcacacgagatccacggttcaagctc 330
QY 387 atacatccatcaatgtgtta 408
DB 331 gtcaatgcttgcgaatgtgatga 352

RESULT 2

AAC45801
ID AAC45801 standard; DNA: 636 Bp.

AC AAC45801;

DT 18-OCT-2000 (first entry)

DE Arabidopsis thaliana DNA fragment SEQ ID NO: 47813.

XX Hybridisation assay; genetic mapping; gene expression control;
XX protein identification; signal transduction pathway;
KM metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

PD 25-FEB-2000; 2000EP-0301439.
XX
PF

XX 25-FEB-1999; 99US-0121825.
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Query Match	30.4%;	Score 124.2;	DB 21;	Length 636;
Best Local Similarity	62.3%;	Pred. No. 8e-30;		
Matches 195;	Conservative	0;	Mismatches 118;	Indels 0;
				Gaps 0.

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Db	58	atgaagttaacaccacaagatgagcctctcttcgcgagaagaacgaagagctcatltnaca	117
QY	156	gcacacatctctgtctcgaacgaatactcatctgtgctgacccctgtcccaaggaactcgaag	215
Db	118	gtcttcctccagaagagacgttgtgtataatgacctctcctctccaccgactcttcgacg	177
QY	216	aaataacaggtctcgtctcttacciatcttcgaaaagaagacgaatcaatcatagttcgcgga	275
Db	178	aagtaacaatgtcatagatcatcatcgtccgatacgaacgcagaggttcacgactcgttcggt	237
QY	276	gtcttcaaggtctagaagaagaaagttltaacaactgttatactgaaagaataatcgtgatacat	335
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QY	336	atcgaagagatgcacgaagaaaacgcgaatcgaatgatcgtctactctgtggtggaatcatcca	395
Db	298	atcgaagagatcacgcgagggagaagatgtgaatgtgaacaacacccgtgaaacgttgtgattcagccg	357
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XX	17-OCT-2000 (first entry)
DT	
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XX Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
PN EP103405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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XX 25-FEB-1999; 99US-0121825.
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Query Match          29.7%; Score 121; DB 21; Length 638;
Best Local Similarity 61.7%; Pred. No. 8.4e-29;
Matches 193; Conservative 0; Mismatches 120; Indels 0; Gaps 0;
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QY 276 gcttcaagggtagagaagaagaattacaacgtgttatcgaagaataatcagatacat 335
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RESULT 4
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 21687.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
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RESULT 10

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XX AAH29813;

XX 27-JUL-2001 (first entry)

XX S cerevisiae apoptosis associated coding sequence YLR325C.

XX Yeast; fungus; apoptosis; infection; proliferative disease;
XX vaccine; autoimmune disease; ischaemia; neurodegeneration; ds.

XX Saccharomyces cerevisiae.

XX W0200102550-A2.

XX 11-JAN-2001.

XX 03-JUL-2000; 2000WO-BE00077.

XX 01-JUL-1999; 99EP-0870141.

XX (JANSEN) JANSSEN PHARM NV.

XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
XX Nelissen BJM, Reekmans RJ;XX WPI: 2001-367042/38.
XX P-PSDB: AAG70777.XX Yeast and fungal nucleic acids encoding proteins involved in a pathway
XX leading to programmed cell death, useful for treating proliferative
XX disorders; yeast and fungal infections, or for preventing apoptosis in
XX certain diseases -

XX Claim 1; Fig 1; 218pp; English.

XX The present invention provides the protein and coding sequences of a
XX number of apoptosis associated proteins from the yeast *Saccharomyces*
XX *cerevisiae* and the fungus *Candida albicans*. These can be used to identify
XX treatments and fungal and yeast infections, for proliferative diseases
XX and for apoptosis related diseases such as autoimmune diseases, ischaemia
XX and neurodegeneration. The present sequence is one of the *S. cerevisiae*
XX coding sequences of the invention.

XX Sequence 1331 BP; 424 A; 234 C; 263 G; 410 T; 0 other;

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XX Best Local Similarity 57.5%; Pred. No. 1.2e-20;
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DB 965 agagcttctccgcagcagaagagcttaagagcttaccgcgccatcccca 1024
QY 170 acagcagatctcagtgagtcacacctgttcacaggaactcagtaagaagcgttcg 229
DB 1025 acgtcgtgttctcgtcgtccatctatcttaaggaagtgagagctcaatcaggtatcaa 1084
QY 230 ttcttaacctcgaagaagaagcagaagtaacatcagtcgcgagcttcacaggtag 289
DB 1085 ggccttgccaatcagaagagatgatgaagtttggtgtcgtcgttcacagaagggtca 1144
QY 290 agagaagaaggttaacacgttgtatcgaagaataatcagatataatcagagaggtac 349
DB 1145 agaaggaaggtatcactcgtttacagatgaattgctccgttcaagttgacaaggttac 1204
QY 350 cagagaaagcgaatgagctgactgactgtggtggaatcaccatcctaatgttgta 408
DB 1205 caaggaagaaggtcaacggtgtcttcgtccatcaactgcaccatccaagcttgta 1263

RESULT 11

AAC03878
ID AAC03878 standard; cDNA; 508 BP.

XX AAC03878;

XX 06-OCT-2000 (first entry)

XX Human secreted protein 5' EST, SEQ ID NO: 3876.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-0200610.

XX 26-FEB-1999; 99US-0122487.

XX (GENET) GENSET.

XX Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.
XX P-PSDB: AAG03872.XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX Claim 1; SEQ ID 3876; 71pp + CD-ROM; English.XX The present sequence is one of a large number of 5' ESTs derived from
XX cDNAs encoding secreted proteins. An ORF has been identified within the
XX sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs
XX derived from 30 different tissues. EST sequences usually correspond
XX mainly to the 3' untranslated region (UTR) of the mRNA because they are
XX often obtained from oligo-dT primed cDNA libraries. Such ESTs are not
XX well suited for isolating cDNA sequences derived from the 5' ends of
XX mRNAs and even in those cases where longer cDNA sequences have been
XX obtained, the full 5' UTR is rarely included. 5' ESTs are derived from
XX mRNAs with intact 5' ends and can therefore be used to obtain full length
XX cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic,
XX gene therapy and chromosome mapping procedures. They are used to obtain
XX upstream regulatory sequences and to design expression and secretion
XX vectors.

XX Sequence 508 BP; 172 A; 113 C; 122 G; 100 T; 1 other;

XX Query Match 22.2%; Score 90.4; DB 21; Length 508;
XX Best Local Similarity 57.6%; Pred. No. 4.3e-19;
XX Matches 182; Conservative 0; Mismatches 131; Indels 3; Gaps 1;

QY 96 atgaatctcaaaagtgtatcgtcgtctagaagaagaaggaagcattcttaa 155
DB 68 atgaagtttaaccccttggtacttcgcagcgaagaagaatcgcgaagaagcattcaat 127
QY 156 gacacatcttcgtacagcgaatcactatgtagtcacccttgcgaagaagctacgttac 215
DB 128 gaaccttcacacatcogaagaagattatgtctccctcttccaagaagctgagacag 187
QY 216 aaatcagaggtgtcttcttactcttcgaagaagaagcagaatcatatggttcggga 275
DB 188 aagtaaaagctgcacatccatccgaagaagatgaaatcaggttcaggttcagtgga 247
QY 276 gcttcaaggtgagagaa---ggaagaattacaacgttgtatcgaagaagaatctcgata 332

Db 248 cactataaaggtcagcaaatgtgcgaagtagtccaggtttacaggaataatggtatc 307
Oy 333 catctcgagaagtgaccacagagaagaacgaatggaatgactgtgactgtggaatacat 392
Db 308 tacattgacggcggtgcgcggaagaagctaatgtgcacaactgtccacgtgacattcac 367
Oy 393 ccatctaattgtgtta 408
Db 368 ccagcaaggtgttga 383

RESULT 12
AAFI5011
ID AAFI5011 standard; cDNA: 785 BP.
AC AAFI5011;
XX 13-MAR-2001 (first entry)
DE Trichoderma reesei EST SEQ ID NO:7534.
XX
XX Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX Trichoderma reesei.
OS
XX WO200056762-A2.
PN 28-SEP-2000.
XX
XX 22-MAR-2000; 2000WO-US07781.
PF
XX 22-MAR-1999; 99US-0273623.
PR
XX (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX WPI: 2000-594572/56.
DR
XX Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags -
XX
PS Claim 89; Page 3043; 3161pp; English.

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAFI5011248 to AAFI1853 represents ESTs from *Fusarium venenatum*; AAFI1248 to AAFI1853 represents ESTs from *Aspergillus niger*; AAFI1854 to AAFI4878 represents ESTs from *Aspergillus oryzae*; and

CC AAFI4878 to AAFI5337 represents ESTs from *Trichoderma reesei*, which are
CC all specifically claimed in the present invention.
XX
SQ Sequence 785 BP; 187 A; 229 C; 193 G; 156 T; 20 other:
Query Match 21.5%; Score 87.8; DB 21; Length 785;
Best Local Similarity 58.5%; Pred. No. 3.4e-18;
Matches 169; Conservative 0; Mismatches 119; Indels 1; Gaps 1;
Oy 115 tctcgtctctagaagaacagagaagcaatacttcaagcaccattcttctgtcagc 174
Db 25 ttctctctccgcgagcaagcagcgtgcctcaactcaagcgcggctgcgcagccg 84
Oy 175 gaatactcagaatgtcaccttggtccaaggaactgaactcaagaatcagcgtgtctt 234
Db 85 gtgtcattcattgagcgcctcccttaagcaagagctgcgcgagaagtcaacagttcgcagaa 144
Oy 235 taacttcgaaagaagacgaagatcatatctgcgcgagcttcaagggtagaagaag 294
Db 145 tcccatccgcaagagcagcagaggtcacctgtcgttggtctcaacaaaggccgtgag 204
Oy 295 gaaagttacaacgtgttatcgaagaataatcggatacatatcgaagaagtgaccagag 354
Db 205 gcaaggtcaccttcgtctaccgcctcaagtaactgtatccacgctgagcgttaccgcgcg 264
Oy 355 aaaaagcgaatggaatgactcctgtgggaatacatcatcatatgt 403
Db 265 acaagcgaagcgcgcagcagcgttnc-ctgggtatccacccctccacgt 312

RESULT 13
AAI39236/c
ID AAI39236 standard; DNA: 472 BP.
XX
XX AAI39236;
AC
XX 17-OCR-2001 (first entry)
DT
XX Probe #7922 used to measure gene expression in human placenta sample.
DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
KW genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200157272-A2.
PN
XX 09-AUG-2001.
PD
XX 30-JAN-2001; 2001WO-US00663.
PF
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632386.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX WPI: 2001-488897/53.
DR
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
PT
XX Claim 25; SEQ ID No 7922; 654pp; English.
XX The present invention relates to single exon nucleic acid probes (SENP).
CC The present sequence is one such probe. The probes are useful for

CC Producing a microarray for predicting, measuring and displaying gene
CC expression in samples derived from human placenta. The probes are useful
CC for antenatal diagnosis of human genetic disorders.
XX
SQ Sequence 472 BP; 105 A; 119 C; 100 G; 148 T; 0 other;

Query Match 19.8%; Score 80.6; DB 22; Length 472;
Best Local Similarity 62.3%; Pred. No. 5,5e-16;
Matches 144; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

QY 181 tctgtgtcacccttgcgaaggaactcgtacgaagaacgcttcttactta 240
Db 468 TCATGTCATCCCGCTCTCCAGAGACTCGGCAGAAATGATGCTCCATGCCCA 409
QY 241 ttgcaaaagaagcgaatcatcgttcgagagcttcaaggttagaaa---gga 297
Db 408 TCCGCAAGACACGACGAGTCCAGGTGTCAGAGACACTCAAGGTCAGCAAAATTGGCA 349
QY 298 aagttcaacgctgtatcgaagaatcgcgatacatcgcagagagtgaccagagaa 357
Db 348 AGTATATCCAGGTACAGAAAGAAATATGTCATCTACATCGAGGGGTCCAGCTGAGA 289
QY 358 aagcgaatggaatgactctgtggaatacatcatcctaagtgtt 408
Db 288 AGGCCAAGCGCAGACTGTCCAGTGGGCATTCAACCAAGAGGTGTTA 238

.RESULT 14

AAc41333
ID AAc41333 standard; DNA; 430 BP.

XX AAC41333;

DE 17-OCT-2000 (first entry)

XX Zea mays DNA fragment SEQ ID NO: 31502.

KW Hybridisation assay; genetic mapping; gene expression control;
KW Protein identification; signal transduction pathway; metabolic;
XX pathway; promoter; termination sequence; corn; ss.

OS Zea mays subsp. mays.

PN EP1033405-A2.

PD 06-SEP-2000.

PE 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 16-APR-1999; 99US-0128714.
PR 19-APR-1999; 99US-0129845.
PR 21-APR-1999; 99US-0130077.
PR 23-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
PR 05-MAY-1999; 99US-0132484.
PR 06-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 07-MAY-1999; 99US-0132487.
PR 11-MAY-1999; 99US-0132863.
PR 99US-0134256.

PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139453.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 02-JUL-1999; 99US-0142154.
PR 06-JUL-1999; 99US-0142055.
PR 08-JUL-1999; 99US-0142390.
PR 09-JUL-1999; 99US-0142803.
PR 12-JUL-1999; 99US-0142920.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144684.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 22-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.

XX Claim 87; Page 1742-1743; 3161pp; English.
PS
YY

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF1247 represents ESTs from *Fusarium venenatum*, AAF11248 to AAF11853 represents ESTs from *Aspergillus niger*, AAF11854 to AAF14878 represents ESTs from *Aspergillus oryzae*, and AAF14879 to AAF15537 represents ESTs from *Trichoderma reesei*, which are all specifically claimed in the present invention.

SQ Sequence 629 BP; 153 A; 191 C; 155 G; 129 T; 1 other;

Query Match	Score	DB	Length
18.08;	73.4;	21;	629;

Matches	146;	Conservative	0;	Mismatches	121;	Indels	0;	Gaps	0;
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[illegible]

